

## SUPPLEMENTAL TABLES

**Table S1, related to Figures 1 and 2.**  
**Crystallographic data collection and refinement statistics**

|   | EREG/sEGFR501     | EPGN/sEGFR501       |
|---|-------------------|---------------------|
| <b>Data collection statistics<sup>a</sup></b> |                   |                     |
| Beamlne                                       | APS 23ID-D        | APS 23ID-B          |
| Wavelength (Å)                                | 1.03              | 1.03                |
| Space group                                   | P2 <sub>1</sub>   | P4 <sub>3</sub> 22  |
| Cell dimensions                               |                   |                     |
| <i>a</i> , <i>b</i> , <i>c</i> (Å)            | 76.6, 199.3, 87.9 | 104.1, 104.1, 285.9 |
| $\alpha$ , $\beta$ , $\gamma$ (°)             | 90.0, 96.7, 90.0  | 90.0, 90.0, 90.0    |
| Resolution (Å)                                | 50.0 – 2.94       | 49.0 – 3.00         |
| Completeness (%)                              | 97.2 (89.8)       | 97.2 (98.8)         |
| Redundancy                                    | 2.8 (2.3)         | 5.3 (5.8)           |
| $R_{\text{sym}}$ (%)                          | 13.1 (45.8)       | 28.0 (65.5)         |
| $l/\sigma$                                    | 8.4 (1.7)         | 6.7 (2.3)           |
| CC <sup>1/2</sup> <sup>b</sup>                | 0.75              | 0.60                |
| <b>Refinement</b>                             |                   |                     |
| Resolution (Å)                                | 47.68 – 2.94      | 48.89 – 3.00        |
| Number of reflections                         | 53,542            | 31,435              |
| $R_{\text{cryst}}/R_{\text{free}}$ (%)        | 22.5 / 26.8       | 26.5 / 31.2         |
| Number of atoms                               |                   |                     |
| Protein                                       | 16,658            | 8,020               |
| Carbohydrate                                  | 404               | 212                 |
| Water   | 41                | 69                  |
| Average B factor (Å <sup>2</sup> )            |                   |                     |
| Protein                                       | 91.9              | 53.3                |
| Carbohydrate                                  | 133.6             | 82.0                |
| Water   | 66.7              | 24.7                |
| Ramachandran favored (%)                      | 94.0              | 92.8                |
| Ramachandran allowed (%)                      | 5.8               | 6.7                 |
| Ramachandran outliers (%)                     | 0.2               | 0.5                 |
| Bond length rmsd (Å)                          | 0.004             | 0.002               |
| Bond angle rmsd (°)                           | 0.902             | 0.654               |
| PDB accession code                            | 5WB7              | 5WB8                |

<sup>a</sup>Numbers in parentheses denote highest resolution shell.

<sup>b</sup>CC<sup>1/2</sup> reported for the highest resolution shell.

**Table S2, related to Figure 5.****Fitting of data from FRET studies of EGFR<sub>ECR-TM-eYFP</sub> fusions**

| Ligand<br>(concentration) | Dimerization $K_d$<br>( $\mu\text{m}^2$ ) $\pm$ S.E. | FRET efficiency<br>$\pm$ S.E. | n   |
|---------------------------|--|-------------------------------|-----|
| EGF (100 nM)              | Constitutive   | $0.40 \pm 0.03$               | 198 |
| EREG (1 $\mu\text{M}$ )   | $63.3 \pm 76.2$                                      | $0.39 \pm 0.04$               | 95  |
| EREG (20 $\mu\text{M}$ )  | $3.74 \pm 8.44$                                      | $0.39 \pm 0.02$               | 274 |
| EPGN (1 $\mu\text{M}$ )   | $494 \pm 273$  | $0.36 \pm 0.04$               | 125 |
| EPGN (20 $\mu\text{M}$ )  | $219 \pm 116$  | $0.38 \pm 0.04$               | 259 |

Data in the absence of ligand did not fit well to a monomer-dimer equilibrium (best-fit values varied depending on the initial values input).